AMENDMENTS TO THE CLAIMS

1. (Withdrawn) A method for analyzing a sugar chain structure, wherein the method comprises the steps of:

(a) introducing a fluorescence-labeled subject sugar chain to an FAC apparatus having parallel columns onto which each of a variety of proteins that interact with a sugar chain are immobilized; and

(b) measuring the interaction of the subject sugar chain with each of the proteins that interact with the sugar chain; wherein

when a combined pattern of a measured interaction of the subject sugar chain with each of the proteins that interact with the sugar chain matches a combined pattern of an interaction of a specific sugar chain with each of the proteins that interact with the sugar chain, taken from control data which comprise the interactions of a number of sugar chains with each of the proteins that interact with the sugar chain, the subject sugar chain is judged to have the same structure as the specific sugar chain.

2. (Withdrawn) The method of claim 1, wherein a protein that interacts with the sugar chain is a lectin, an enzymatic protein comprising a sugar-binding domain, a cytokine having affinity for a sugar chain, or an antibody that interacts with a sugar chain.

3. (Withdrawn) A system for analyzing a sugar chain structure using a computer and comprising:

(a) a storage means which stores data on the interaction of a number of sugar chains with a variety of proteins that interact with a sugar chain;

(b) a detection means which, when a fluorescence-labeled subject sugar chain is introduced into an FAC apparatus having parallel columns onto which each of the various proteins that interact with sugar chains is immobilized, detects the fluorescence intensity over time of a label attached to a subject sugar chain eluted from each column;

(c) a means for calculating data on the interaction of a subject sugar chain with each of the proteins that interact with sugar chains, based on an entered fluorescence intensity data, comparing a data combination of said interaction data with a data combination stored in (a), and

selecting one or a number of sugar chains of known structure having a matching data combination pattern; and,

(d) a display means for displaying the selection results.

4. (Withdrawn) The system of claim 3, wherein the arithmetic processing means of step (c) comprises the following (i) or (ii):

(i) a means for calculating the elution volume of a subject sugar chain from each column based on an entered fluorescence intensity data, calculating a difference between said elution volume and a control elution volume, comparing a data combination of said difference with a data combination stored in (a), and selecting one or a number of sugar chains of known structure having a matching data combination pattern; or,

(ii) a means for calculating the elution volume of a subject sugar chain from each column based on an entered fluorescence intensity data, calculating a difference between said elution volume and a control elution volume, calculating an affinity constant for the subject sugar chain with each of the proteins that interact with sugar chains based on said difference, comparing a data combination of said affinity constant with data combination stored in (a), and selecting one or a number of sugar chains of known structure having a matching data combination pattern.

5. (Withdrawn) The system of claim 3, wherein a protein that interacts with a sugar chain is a lectin, an enzymatic protein having a sugar-binding domain, a cytokine having an affinity for a sugar chain, or an antibody that interacts with a sugar chain.

6. (Original) A method for analyzing a sugar chain structure, wherein the method comprises:

(a) a step of contacting a fluorescence-labeled subject sugar chain with a substrate onto which each of a variety of proteins that interact with a sugar chain is immobilized; and

(b) a step of measuring the interaction of the subject sugar chain with each of the proteins that interact with the sugar chain by allowing an excitation light to act without carrying out a washing operation; wherein

when a combined pattern of a measured interaction of the subject sugar chain with each of the proteins that interact with the sugar chain matches a combined pattern of an interaction of a

specific sugar chain with each of the proteins that interact with the sugar chain, taken from control data which comprise the interactions of a number of sugar chains with each of the proteins that interact with the sugar chain, the subject sugar chain is judged to have the same structure as the specific sugar chain.

7. (Original) The method of claim 6, wherein the excitation light is an evanescent wave.

8. (Previously Presented) The method of claim 6, wherein a protein that interacts with a sugar chain is a lectin, an enzymatic protein having a sugar-binding domain, a cytokine having an affinity for a sugar chain, or an antibody that interacts with a sugar chain.

9. (Currently Amended) A system for analyzing a sugar chain structure using a computer and comprising:

(a) a ~~storage means~~ database which stores data on the interaction of a number of sugar chains with a variety of proteins that interact with a sugar chain; and

(b) a ~~detection means~~ fluorescence detector which, when a fluorescence-labeled subject sugar chain is contacted with a substrate onto which each of the various proteins that interact with sugar chains are immobilized, detects the intensity of an excited fluorescence after an incident excitation light has been shone on the substrate, without carrying out a washing procedure;

wherein the computer is configured for:

~~(c) a means for~~ taking a data combination of the detected fluorescence intensity, comparing it with data stored in (a), and selecting one or a number of sugar chains of known structure having a matching data combination pattern~~; and~~ .

~~(d) a display means for displaying the selection results.~~

10. (Original) The system of claim 9, wherein the excitation light is an evanescent wave.

11. (Previously Presented) The system of claim 9, wherein a protein that interacts with a sugar chain is a lectin, an enzymatic protein having a sugar-binding domain, a cytokine having an affinity for a sugar chain, or an antibody that interacts with a sugar chain.

12. (New) The method of claim 6, wherein said step of contacting a fluorescence-labeled subject sugar chain with a substrate occurs in a frontal affinity chromatography (FAC) apparatus having parallel columns.

13. (New) The system of claim 9, further comprising a frontal affinity chromatography (FAC) apparatus having parallel columns, wherein said FAC contains each of the various proteins that interact with sugar chains are immobilized on the column.

14. (New) The system of claim 9, wherein the computer is configured for:
(i) calculating the elution volume of a subject sugar chain from each column based on an entered fluorescence intensity data, calculating a difference between said elution volume and a control elution volume, comparing a data combination of said difference with a data combination stored in said database, and selecting one or a number of sugar chains of known structure having a matching data combination pattern; or,
(ii) calculating the elution volume of a subject sugar chain from each column based on an entered fluorescence intensity data, calculating a difference between said elution volume and a control elution volume, calculating an affinity constant for the subject sugar chain with each of the proteins that interact with sugar chains based on said difference, comparing a data combination of said affinity constant with data combination stored in said database, and selecting one or a number of sugar chains of known structure having a matching data combination pattern.